



SEQUENCE LISTING

<110> SATO, TSUYOSHI
OKUDA, MITSUYOSHI
KOYAMA, SHINGO
IZAWA, YOSHIFUMI
KOBAYASHI, TOHRU

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<140> US 10/820/712

<141> 2004-04-09

<150> JP 2003-106708

<151> 2003-04-10

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<170> PatentIn version 3.3

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Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
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115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
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Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
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Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
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225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

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275 280 285

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 Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
 325 330 335
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 Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
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Asn Asn Ala Asn Asp Thr Asn Gly His Gly Thr His Val Ala Gly Ser	
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Val Leu Gly Asn Gly Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn	
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Pro Ser Asn Leu Gln Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala	
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Pro Asp Ser Ser Phe Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met	
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-110

-105

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Val Met Ala Pro Gly Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala
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Gly Gly Thr Ser Met Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln
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Tyr Pro Asn Gly Asn Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser
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320 325 330

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365 370 375

Tyr Val Gly Asn Asp Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly
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Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr
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 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
 20 25 30

 ttg gat aca gga aga aac gac agt tcg atg cat gaa gcc ttc cgc ggt 144
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 35 40 45

 aaa ata aca gca cta tat gca ctg ggt cgg acg aat aat gcg aat gat 192
 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 50 55 60

 acg aac ggt cat ggt acc cat gtg gca ggt tcg gta tta gga aat ggc 240
 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
 65 70 75 80

 gca acg aat aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc 288

Ala	Thr	Asn	Lys	Gly 85	Met	Ala	Pro	Gln	Ala 90	Asn	Leu	Val	Phe	Gln 95	Ser		
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Ile	Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Gln		
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acc	tta	ttc	agc	caa	gca	ttc	agt	gca	ggg	gcc	aga	att	cat	aca	aac		384
Thr	Leu	Phe	Ser	Gln	Ala	Phe	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn		
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tcc	tgg	ggg	gca	gcg	gtg	aat	ggg	gcc	tac	acg	aca	gat	tcc	aga	aat		432
Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn		
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Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala		
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Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala		
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aaa	aac	gcc	atc	act	gtc	ggc	gca	acc	gaa	aac	ctg	cgt	cca	agc	ttc		576
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe		
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ggg	tcc	tat	gca	gat	aat	att	aac	cac	gtt	gca	cag	ttc	tct	tcc	cgt		624
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg		
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Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly		
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Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met		
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Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe		
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Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr	
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Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr	
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Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu	
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gat ttg gtc att aca gca cca aac gga aca aga tat gtc ggg aat gac	1152
Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp	
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Phe Ser Ala Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu	
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Asn Val Phe Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val	
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Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
 65 70 75 80

Ala Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
 85 90 95

Ile Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
 100 105 110

Thr Leu Phe Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn
 115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
 130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
 145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
 165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
 180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
 195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
 210 215 220

Thr Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
 225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
 245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
 260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
 275 280 285

Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
 305 310 315 320

Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp
 370 375 380

Phe Ser Ala Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile

420

425

430

Val Asn

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 <211> 1302
 <212> DNA
 <213> Bacillus sp. KSM-9865

<220>
 <221> CDS
 <222> (1)..(1302)

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 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
 1 5 10 15
 tac ggg ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg 96
 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
 20 25 30
 ctt gat aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgg ggg 144
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 35 40 45
 aaa att act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat 192
 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 50 55 60
 acg aat ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc 240
 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
 65 70 75 80
 tcc act aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct 288
 Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
 85 90 95
 atc atg gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa 336
 Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
 100 105 110
 acc tta ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac 384
 Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
 115 120 125
 tcc tgg gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat 432

Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn	
130						135					140					
gtg	gat	gac	tat	gtg	cgc	aaa	aat	gat	atg	acg	atc	ctt	ttc	gct	gcc	480
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala	
145					150					155					160	
ggg	aat	gaa	gga	ccg	aac	ggc	gga	acc	atc	agt	gca	cca	ggc	aca	gct	528
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	
				165					170					175		
aaa	aat	gca	ata	aca	gtc	gga	gct	acg	gaa	aac	ctc	cgc	cca	agc	ttc	576
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe	
			180					185					190			
ggg	tct	tat	gcg	gac	aat	atc	aac	cat	gtg	gca	cag	ttc	tct	tca	cgt	624
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	
		195					200					205				
gga	ccg	aca	aag	gat	gga	cgg	atc	aaa	ccg	gat	gtc	atg	gca	ccg	gga	672
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	
	210					215					220					
acg	ttc	ata	cta	tca	gca	aga	tct	tct	ctt	gca	ccg	gat	tcc	tcc	ttc	720
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	
225					230					235					240	
tgg	gcg	aac	cat	gac	agt	aaa	tat	gca	tac	atg	ggc	gga	acg	tcc	atg	768
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	
				245					250					255		
gct	aca	ccg	atc	gtt	gct	gga	aac	gtg	gca	cag	ctt	cgt	gag	cat	ttt	816
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	
			260					265					270			
gtg	aaa	aac	aga	ggc	atc	aca	cca	aag	cct	tct	cta	tta	aaa	gcg	gca	864
Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	
		275					280					285				
ctg	att	gcc	ggc	gca	gca	gac	atc	ggc	ctt	ggc	tac	ccg	aac	ggc	aac	912
Leu	Ile	Ala	Gly	Ala	Ala	Asp	Ile	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn	
	290					295					300					
caa	gga	tgg	gga	cga	gtg	aca	ttg	gat	aaa	tcc	cta	aac	gtt	gcc	tat	960
Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	
305					310					315					320	
gtg	aac	gag	tcc	agt	tct	cta	tcc	acc	agc	caa	aaa	gcg	acg	tac	tcg	1008
Val	Asn	Glu	Ser	Ser	Ser	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Ser	
				325					330					335		

ttt act gct act gcc ggc aag cct ttg aag atc tcc ctg gta tgg tct	1056
Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser	
340 345 350	

gat gcc cct gcg agc aca act gct tcc gta acg ctt gtc aat gac ctg	1104
Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu	
355 360 365	

gac ctt gtc att acc gct cca aat ggc aca caa tat gtt gga aat gac	1152
Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp	
370 375 380	

ttt act tcg cca tac aat aat aac tgg gat ggc cgc aat aac gta gaa	1200
Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu	
385 390 395 400	

aat gta ttt att aat gcg cca caa agc ggg acg tat aca att gag gta	1248
Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val	
405 410 415	

cag gct tat aac gta ccg gtt gga cca cag acc ttc tcg ttg gca att	1296
Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile	
420 425 430	

gtg aac	1302
Val Asn	

<210> 14
 <211> 434
 <212> PRT
 <213> Bacillus sp. KSM-9865

<400> 14

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser
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Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
65 70 75 80

Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
85 90 95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
 275 280 285

Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
 305 310 315 320

Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
 370 375 380

Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile
 420 425 430

Val Asn

<210> 15
 <211> 1299
 <212> DNA
 <213> Bacillus sp. D-6

<220>

<221> CDS

<222> (1)..(1299)

<400> 15

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1				5					10					15		

tac	gga	cta	tat	gga	caa	ggt	caa	gta	gtt	gca	gta	gcg	gat	acg	ggt	96
Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly	
			20					25					30			

tta	gat	aca	ggt	cgt	aac	gat	agt	tct	atg	cat	gaa	gca	ttc	cgt	ggg	144
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly	
		35					40					45				

aaa	att	aca	gct	ctt	tac	gcg	tta	gga	aga	act	aac	aat	gca	aat	gat	192
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp	
	50					55					60					

ccg	aat	ggg	cat	ggt	acg	cat	gta	gct	ggt	tct	gtg	ctt	ggt	aat	gct	240
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala	
65					70					75					80	

tta	aat	aaa	gga	atg	gct	ccg	caa	gct	aac	tta	gtc	ttc	caa	tct	att	288
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile	
				85					90					95		

atg	gat	agc	agc	gga	gga	tta	gga	gga	tta	cca	tcg	aat	tta	aat	acg	336
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr	
			100					105					110			

tta	ttt	agt	caa	gct	tgg	aat	gct	ggc	gct	aga	att	cat	act	aac	tct	384
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser	
		115					120					125				

tgg	ggg	gcc	cca	gta	aat	gga	gcg	tac	act	gct	aac	tcg	aga	caa	gtg	432
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val	
	130					135					140					

gat	gag	tat	gtt	cga	aac	aat	gat	atg	acg	gta	ctt	ttt	gca	gct	gga	480
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly	
145					150					155					160	

aat	gaa	gga	cct	aac	tct	gga	aca	att	agc	gct	cca	ggg	aca	gcg	aaa	528
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys	
				165					170					175		

aat	gcc	att	acg	gtc	ggc	gca	acg	gaa	aac	tac	cga	cca	agt	ttt	ggt	576
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Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly	
			180					185					190			
tca	att	gca	gat	aac	cct	aat	cat	atc	gca	caa	ttt	tca	tcg	aga	gga	624
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly	
		195					200					205				
gct	acg	aga	gat	gga	cga	att	aaa	cca	gac	gta	aca	gct	cct	gga	aca	672
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr	
	210					215					220					
ttt	ata	tta	tca	gca	cgc	tct	tct	tta	gca	cca	gac	tct	tcg	ttt	tgg	720
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	
225					230					235					240	
gcg	aat	tat	aac	agt	aag	tat	gcg	tat	atg	ggc	ggt	acc	tct	atg	gcg	768
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	
				245					250					255		
aca	cct	ata	gtt	gcg	ggg	aat	gtc	gcg	caa	tta	cgc	gag	cat	ttt	ata	816
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile	
			260					265					270			
aaa	aat	aga	gga	att	aca	cct	aaa	cct	tcc	tta	ata	aaa	gct	gca	ctt	864
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu	
		275					280					285				
atc	gct	ggg	gct	act	gat	gtt	ggg	tta	gga	tat	cca	agt	ggg	gac	caa	912
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln	
	290					295					300					
ggc	tgg	ggg	cgt	gtt	act	tta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc	960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	
305					310					315					320	
aat	gaa	gca	act	gca	tta	aca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008
Asn	Glu	Ala	Thr	Ala	Leu	Thr	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe	
				325					330					335		
caa	acg	caa	gcg	ggg	aaa	cca	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat	1056
Gln	Thr	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp	
			340					345					350			
gca	cct	gga	agt	aca	aca	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat	1104
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp	
		355					360					365				
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	ggg	aat	gat	ttt	1152
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe	
	370					375					380					

agt	tat	cct	tat	gat	aat	aat	tgg	gat	ggt	cgc	aac	aat	ggt	gag	aac	1200
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn	
385					390					395					400	

gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	ggt	caa	1248
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln	
				405					410						415	

gcg	tat	aac	ggt	cca	tct	gga	cca	cag	cgt	ttc	tca	cta	gct	atc	gta	1296
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val	
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cat																1299
His																

<210> 16
 <211> 433
 <212> PRT
 <213> Bacillus sp. D-6

<400> 16

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Asn	Asn
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Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly
			20					25					30		

Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly
		35					40					45			

Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp
	50					55					60				

Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala
65					70					75					80

Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile
				85					90					95	

Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr
			100					105						110	

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
180 185 190

Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
305 310 315 320

Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe
 325 330 335

Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
 340 345 350

/
 Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

<210> 17
 <211> 1299
 <212> DNA
 <213> Bacillus sp. Y

<220>
 <221> CDS
 <222> (1)..(1299)

<400> 17
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 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
 1 5 10 15

tac gga tta tat gga caa ggt caa gta gtt gca gta gcg gac aca ggc 96
 Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly

20						25						30						
tta	gat	aca	ggt	cgt	aac	gat	agt	tct	atg	cat	gaa	gca	ttc	cgc	ggg	144		
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly			
		35					40					45						
aaa	atc	aca	gct	ctt	tac	gcg	tta	gga	aga	act	aat	aat	gcg	agt	gat	192		
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Ser	Asp			
	50					55					60							
ccg	aat	ggg	cat	ggc	aca	cat	gta	gca	ggt	tct	gta	ctt	ggt	aat	gct	240		
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala			
65					70					75					80			
tta	aat	aaa	gga	atg	gct	ccg	caa	gct	aac	tta	gtc	ttc	caa	tct	att	288		
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile			
				85					90					95				
atg	gat	agc	agc	gga	gga	tta	ggt	ggc	tta	cca	tcg	aac	tta	aat	acg	336		
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr			
			100					105					110					
tta	ttt	agt	caa	gct	tgg	aat	gct	gga	gca	aga	att	cat	act	aac	tct	384		
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser			
		115					120					125						
tgg	gga	gcc	cca	gta	aat	gga	gcg	tac	act	gct	aac	tcg	aga	caa	gtg	432		
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val			
	130					135					140							
gat	gaa	tat	gtt	cga	aat	aat	gat	atg	acg	gta	ctt	ttt	gca	gct	ggt	480		
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly			
145					150					155					160			
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Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys			
				165					170					175				
aat	gct	att	acg	gtc	ggc	gca	acg	gaa	aac	tat	cgc	cca	agc	ttc	ggt	576		
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly			
			180					185					190					
tcg	ata	gca	gat	aac	cca	aat	cat	att	gca	caa	ttt	tca	tcg	aga	gga	624		
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly			
		195					200					205						
gct	acg	agg	gat	gga	cga	att	aag	cct	gac	gta	aca	gct	cct	gga	aca	672		
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr			
	210					215					220							
ttt	att	tta	tca	gca	cgt	tct	tcc	tta	gct	cca	gac	tct	tcg	ttt	tgg	720		

Phe 225	Ile	Leu	Ser	Ala	Arg 230	Ser	Ser	Leu	Ala	Pro 235	Asp	Ser	Ser	Phe	Trp 240	
gcg Ala	aat Asn	tat Tyr	aac Asn	agt Ser	aaa Lys	tac Tyr	gcg Ala	tat Tyr	atg Met	ggc Gly	ggt Gly	acc Thr	tcc Ser	atg Met	gcg Ala	768
aca Thr	cct Pro	att Ile	gtt Val	gca Ala	ggg Gly	aat Asn	gtc Val	gcg Ala	caa Gln	tta Leu	cgt Arg	gag Glu	cat His	ttt Phe	ata Ile	816
aaa Lys	aat Asn	aga Arg	ggg Gly	att Ile	act Thr	cct Pro	aag Lys	cct Pro	tct Ser	tta Leu	ata Ile	aaa Lys	gct Ala	gca Ala	ctt Leu	864
atc Ile	gct Ala	ggg Gly	gct Ala	act Thr	gat Asp	gtt Val	ggg Gly	tta Leu	gga Gly	tat Tyr	cct Pro	aat Asn	ggg Gly	gac Asp	caa Gln	912
ggc Gly	tgg Trp	ggg Gly	cgt Arg	gtt Val	act Thr	cta Leu	aat Asn	aaa Lys	tcg Ser	tta Leu	aat Asn	gta Val	gcg Ala	tat Tyr	gtc Val	960
aat Asn	gaa Glu	gca Ala	act Thr	gca Ala	tta Leu	gcc Ala	aca Thr	gga Gly	caa Gln	aaa Lys	gca Ala	acg Thr	tat Tyr	tcg Ser	ttc Phe	1008
caa Gln	gca Ala	caa Gln	gcg Ala	ggg Gly	aaa Lys	cct Pro	tta Leu	aaa Lys	atc Ile	tcg Ser	tta Leu	gta Val	tgg Trp	aca Thr	gat Asp	1056
gct Ala	cct Pro	gga Gly	agt Ser	aca Thr	act Thr	gca Ala	tct Ser	tat Tyr	aca Thr	cta Leu	gtt Val	aat Asn	gat Asp	tta Leu	gat Asp	1104
cta Leu	gtt Val	att Ile	act Thr	gct Ala	ccg Pro	aat Asn	gga Gly	caa Gln	aaa Lys	tat Tyr	gta Val	gga Gly	aat Asn	gat Asp	ttt Phe	1152
agt Ser	tat Tyr	cct Pro	tat Tyr	gat Asp	aat Asn	aac Asn	tgg Trp	gat Asp	ggg Gly	cgc Arg	aac Asn	aat Asn	gtt Val	gag Glu	aac Asn	1200
gta Val	ttt Phe	ata Ile	aac Asn	gct Ala	ccg Pro	caa Gln	tct Ser	gga Gly	acg Thr	tat Tyr	ata Ile	att Ile	gag Glu	gtt Val	caa Gln	1248
gcg Ala	tat Tyr	aat Asn	gta Val	cca Pro	tct Ser	ggc Gly	cca Pro	cag Gln	cgt Arg	ttc Phe	tca Ser	cta Leu	gct Ala	atc Ile	gta Val	1296

cat
His

1299

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<211> 433
<212> PRT
<213> Bacillus sp. Y

<400> 18

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20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
145 150 155 160

Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys
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			180					185					190		
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly
		195					200					205			
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr
	210					215					220				
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp
225					230					235					240
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala
				245					250					255	
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile
			260					265					270		
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu
		275					280					285			
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asp	Gln
	290					295					300				
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asn	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val
305					310					315					320
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe
				325					330					335	
Gln	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp
			340					345					350		
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp
		355					360					365			

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
 420 425 430

His

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 <211> 1299
 <212> DNA
 <213> Bacillus SD521

<220>
 <221> CDS
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tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt	96
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly	
20 25 30	
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg	144
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly	
35 40 45	
aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat	192
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp	
50 55 60	
ccg aat ggg cat ggt acg cat gta gca ggt tct gta ctt ggt aat gct	240
Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala	

65	70					75					80					
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att																288
Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile																
	85					90					95					
atg gat agc agc gga gga tta ggt gga tta cca tcg aat ttg aat acg																336
Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr																
	100					105					110					
tta ttt agt caa gct tgg aat gct ggg gct aga att cat act aac tct																384
Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser																
	115					120					125					
tgg ggt gct cca gta aat gga gcg tac act gct aac tcg aga caa gtg																432
Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val																
	130					135					140					
gat gag tat gtt cga aat aat gat atg acg gta ctt ttt gca gca ggt																480
Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly																
	145					150					155					160
aat gaa ggt cct aat tca gga aca att agt gct cca ggc aca gcg aaa																528
Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys																
	165					170					175					
aat gcc att acg gtc ggc gca acg gaa aac tat cgc ccg agc ttc ggt																576
Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly																
	180					185					190					
tca tta gca gat aac cca aat cat atc gca caa ttt tca tca aga gga																624
Ser Leu Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly																
	195					200					205					
gct acg aga gat gga cga att aaa cca gac gta aca gct cct gga aca																672
Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr																
	210					215					220					
ttt att tta tca gca cgt tct tcc tta gcc cca gac tct tcg ttt tgg																720
Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp																
	225					230					235					240
gcg aat tat aac agt aag tat gcg tac atg ggc ggt acc tct atg gcg																768
Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala																
	245					250					255					
aca cct ata gtt gcg ggg aat gtc gcg caa tta cgc gag cat ttt ata																816
Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile																
	260					265					270					
aaa aat aga gga att aca cct aaa cct tcc tta ata aaa gct gca ctt																864

Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu		
		275					280					285					
atc	gct	ggg	gct	act	gat	gtt	ggg	tta	gga	tat	cca	agt	ggg	gac	caa		912
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln		
	290					295					300						
ggc	tgg	ggg	cgt	gtt	act	cta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc		960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val		
305					310					315					320		
aat	gaa	gca	act	gca	tta	gca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc		1008
Asn	Glu	Ala	Thr	Ala	Leu	Ala	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe		
				325					330					335			
caa	gca	caa	gcg	ggg	aaa	cct	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat		1056
Gln	Ala	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp		
			340					345					350				
gca	cct	gga	agt	aca	act	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat		1104
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp		
		355					360					365					
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	gga	aat	gat	ttt		1152
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe		
	370					375					380						
agt	tat	cct	tat	gat	aat	aac	tgg	gat	ggg	cgc	aac	aat	gtt	gag	aac		1200
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn		
385					390					395					400		
gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	gtt	caa		1248
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln		
				405				410						415			
gcg	tat	aat	gta	cca	tct	ggc	cca	cag	cgt	ttc	tca	cta	gct	atc	gta		1296
Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val		
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cat																	1299
His																	

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 <211> 433
 <212> PRT
 <213> Bacillus SD521

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			20					25					30			
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly	
		35					40					45				
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp	
	50					55					60					
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala	
65					70					75					80	
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile	
				85					90					95		
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr	
			100					105					110			
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser	
		115					120					125				
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val	
	130					135					140					
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly	
145					150					155					160	
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys	
				165					170					175		
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly	
			180					185					190			
Ser	Leu	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly	
		195					200					205				

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe
325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe
370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
405 410 415

Ala	Tyr	Asn	Val	Pro	Ser	Gly	Pro	Gln	Arg	Phe	Ser	Leu	Ala	Ile	Val
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His

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 <212> DNA
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1				5					10					15						
tat	ggt	tta	tat	ggg	caa	ggg	caa	gtg	ggt	gca	gta	gcg	gat	acc	gga					96
Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly					
			20					25					30							
ctg	gat	aca	ggg	cgt	aat	gac	agc	tcg	atg	cat	gaa	gcg	ttc	cga	gga					144
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly					
		35				40						45								
aag	att	acc	gcg	ata	tat	gcc	ctt	gga	aga	aca	aac	aac	gcc	aat	gat					192
Lys	Ile	Thr	Ala	Ile	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp					
	50					55					60									
cca	aac	gga	cac	ggg	acg	cat	ggt	gcc	gga	tct	ggt	tta	gga	aac	ggt					240
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly					
65				70					75					80						
act	tcg	aat	aaa	ggg	atg	gct	cca	caa	gct	aac	tta	ggt	ttc	caa	tct					288
Thr	Ser	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser					
			85					90					95							
ggt	atg	gac	agc	aat	ggc	gga	ctt	ggc	gga	ctg	cct	tcc	aat	gta	agt					336
Val	Met	Asp	Ser	Asn	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Val	Ser					
			100					105					110							
aca	tta	ttc	agc	cag	gca	tat	agt	gcc	ggt	gcc	aga	atc	cat	acg	aac					384
Thr	Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn					

115					120					125									
tca	tgg	gga	gcg	cct	gta	aac	gga	gcg	tac	act	act	gat	tcc	aga	aac	432			
Ser	Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn				
130					135					140									
gta	gac	gat	tat	gtt	cgt	aaa	aat	gat	atg	gcg	gtt	ctt	ttt	gca	gcg	480			
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Ala	Val	Leu	Phe	Ala	Ala				
145					150					155					160				
ggt	aac	gaa	ggg	ccg	aat	ggc	ggc	aca	atc	agt	gct	cct	ggt	acc	gcg	528			
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala				
165					170					175									
aag	aat	gct	atc	aca	gta	ggg	gca	aca	gaa	aac	ctg	cgc	cca	agc	ttt	576			
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe				
180					185					190									
gga	tct	tat	gct	gac	aac	atc	aat	cat	gta	gca	cag	ttt	tcc	tcc	cgc	624			
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg				
195					200					205									
gga	cct	aca	aag	gat	gga	cgt	atc	aaa	ccg	gac	gta	atg	gca	cca	gga	672			
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly				
210					215					220									
aca	ttt	att	tta	tcg	gca	aga	tct	tct	ttg	gct	ccg	gac	tcc	tca	ttc	720			
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe				
225					230					235					240				
tgg	gca	aac	cat	gac	agc	aaa	tat	gct	tat	atg	ggt	gga	aca	tcc	atg	768			
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met				
245					250					255									
gcg	aca	ccg	att	gta	gct	ggt	aac	gtt	gca	cag	tta	cgt	gaa	cat	ttc	816			
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe				
260					265					270									
atc	aaa	aac	aga	gga	atc	act	cct	aaa	cca	tcc	ttg	ctg	aaa	gca	gct	864			
Ile	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala				
275					280					285									
ctt	att	gcc	gga	gca	act	gat	atc	ggt	ctt	ggc	tat	ccg	agt	gga	aac	912			
Leu	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asn				
290					295					300									
caa	gga	tgg	gga	aga	gta	aca	ttg	gac	aag	tca	ctt	aat	gta	gct	ttc	960			
Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Phe				
305					310					315					320				
gta	aat	gaa	aca	agc	tct	tta	tct	act	aac	caa	aag	gct	acg	tat	tca	1008			

Val	Asn	Glu	Thr	Ser	Ser	Leu	Ser	Thr	Asn	Gln	Lys	Ala	Thr	Tyr	Ser		
				325					330					335			
ttt	act	gca	caa	tca	ggc	aaa	cct	ttg	aag	att	tca	ttg	gtt	tgg	tct	1056	
Phe	Thr	Ala	Gln	Ser	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser		
			340					345					350				
gat	gca	ccg	gca	agt	act	tcc	gca	tcg	gtt	aca	ttg	gtg	aat	gat	ctg	1104	
Asp	Ala	Pro	Ala	Ser	Thr	Ser	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu		
		355					360					365					
gat	ctg	gtg	att	aca	gct	cca	aat	gga	aca	aag	tat	gtt	gga	aac	gac	1152	
Asp	Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Thr	Lys	Tyr	Val	Gly	Asn	Asp		
	370					375					380						
ttt	act	gct	ccc	tat	gat	aat	aac	tgg	gat	gga	cgt	aac	aat	gta	gag	1200	
Phe	Thr	Ala	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu		
385					390					395				400			
aac	gtg	ttt	atc	aat	gct	ccg	caa	agc	gga	acg	tat	aca	gtt	gag	gta	1248	
Asn	Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Val	Glu	Val		
				405					410					415			
cag	gct	tac	aat	gtt	cca	caa	ggg	ccg	cag	gcg	ttt	tct	ttg	gct	att	1296	
Gln	Ala	Tyr	Asn	Val	Pro	Gln	Gly	Pro	Gln	Ala	Phe	Ser	Leu	Ala	Ile		
			420					425					430				
gtg	aac															1302	
Val	Asn																

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 <212> PRT
 <213> NCIB12289

<400> 22

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Ser	Ser		
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Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly		
			20					25					30				
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly		
		35					40					45					

Lys Ile Thr Ala Ile Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
 65 70 75 80

Thr Ser Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
 85 90 95

Val Met Asp Ser Asn Gly Gly Leu Gly Gly Leu Pro Ser Asn Val Ser
 100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
 115 120 125

Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
 130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala
 145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
 165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
 180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
 195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
 210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
 225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
 245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
260 265 270

Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
275 280 285

Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn
290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe
305 310 315 320

Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser
325 330 335

Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
340 345 350

Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu
355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp
370 375 380

Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val
405 410 415

Gln Ala Tyr Asn Val Pro Gln Gly Pro Gln Ala Phe Ser Leu Ala Ile
420 425 430

Val Asn

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<212> PRT
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Phe Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
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Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
65 70 75 80

Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
85 90 95

Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ala Asn Leu Gln Thr
100 105 110

Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn Ser
115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn Val
130 135 140

Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala Gly
145 150 155 160

Asn Glu Gly Pro Gly Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
165 170 175

Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe Gly
180 185 190

Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg Gly
195 200 205

Pro Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly Thr
210 215 220

Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
225 230 235 240

Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Val
260 265 270

Lys Asn Arg Gly Val Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala Leu
275 280 285

Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Phe Pro Asn Gly Asn Gln
290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe Val
305 310 315 320

Asn Glu Thr Ser Pro Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe
325 330 335

Thr Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp
340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Leu Thr Leu Val Asn Asp Leu Asp
355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp Phe
370 375 380

Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn

385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val Gln
405 410 415

Ala Tyr Asn Val Pro Val Ser Pro Gln Thr Phe Ser Leu Ala Ile Val
420 425 430

His

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<212> PRT
<213> Artificial Sequence

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Gly Ala Ala Pro Leu
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